

(without alignments)
1495.730 Million cell updates/sec

Sequence: 1 MKQILHPAETTTAMTLFVL.....KHQLVRDSCCKASCNCNSIY 256

Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

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Command line parameters:
-MODEL=framed_p2n_model -DEV=xlh
-Q=/cgen.1/USPRO.spool/US09698781/runat_07032003_083458.5317/app_query.fasta.1.6554
DB=NGeneSeq.101002 -OPMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOCP=0
-LIST=45 -UNITS=bits -START=1 -END=1 -MATRIX=10sums6 -TRANS=huffman40.cdl
-LIO=45 -DOCALLIG=200 -THR SCORE=0 -THR SCORE=0 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=PCO -NORM=ext -HEAPSIZE=500 -MILEN=0 -MAXLEN=2000000000
-USER=US09698781 -GCN=1.1.338 -tunat_07032003_083458.5317 -NCPU=6 -ICPU=3
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-WARN=TIMCOUT=30 -THRADS=1 -XGAP=10 -XGAPEXT=0.5 -FGAP=6 -FGAPEXT=7
-YGAP=0 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1981.DAT *
3:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1982.DAT *
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6:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1985.DAT *
7:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1986.DAT *
8:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1987.DAT *
9:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1988.DAT *
10:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1989.DAT *
11:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1990.DAT *
12:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1991.DAT *
13:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1992.DAT *
14:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1993.DAT *
15:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1994.DAT *
16:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1995.DAT *
17:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1996.DAT *
18:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1997.DAT *
19:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1998.DAT *
20:	/SDS2/gcgdata/genseq/genseqn-emb1/NA1999.DAT *
21:	/SDS2/gcgdata/genseq/genseqn-emb1/NA2000.DAT *
22:	/SDS2/gcgdata/genseq/genseqn-emb1/NA2001A.DAT *
23:	/SDS2/gcgdata/genseq/genseqn-emb1/NA2001B.DAT *
24:	/SDS2/gcgdata/genseq/genseqn-emb1/NA2002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result	Score	Match	Query	Length	DB	ID	Description
No.							
1	1436	100	0	2144	22	AAD063222	Human full-length
2	1433	99.8		1610	23	ABV24823	Human prostate exp
3	1428	99.4		2133	22	AAH98651	Human EST-derived
4	1428	99.4		2133	22	AAH98659	Human EST-derived
5	1428	99.4		2452	23	ABV22644	Human prostate exp
6	1428	99.4		2452	23	ABV24631	Human prostate exp
7	1428	99.4		2452	23	ABV25272	Human prostate exp
8	1428	99.4		2452	23	ABV23706	Human prostate exp
9	1428	99.4		2452	23	ABV28467	Human prostate exp
10	1428	99.4		2452	23	ABV28648	Human prostate exp
11	1386	96.5		2128	24	ABL67806	Oesophagus cancer
12	1002	69.8		1386	23	AAST0843	DNA encoding novel
13	1002	69.8		1386	23	AAST9411	DNA encoding novel
14	683	47.6		534	23	ABV43214	Human prostate exp
15	535.5	37.3		683	23	AAST0842	DNA encoding novel
16	535.5	37.3		683	23	AAST9408	DNA encoding novel
17	500	34.8		372	23	ABV13234	Human prostate exp
18	494	34.4		395	23	ABV34353	Human prostate exp
19	400.5	27.9		395	23	ABV38239	Human prostate exp
20	400	27.9		340	23	ABV08906	Human prostate exp
21	399	27.8		543	23	ABV08331	Human prostate exp
22	397	27.6		430	23	ABV08865	Human prostate exp
23	397	27.6		451	23	ABV38756	Human prostate exp
24	396	27.6		400	23	ABV07202	Human prostate exp
25	396	27.6		633	23	ABV37142	Human prostate exp
26	356.5	24.8		530	23	ABV38795	Human prostate exp
27	354	24.7		263	20	AAAX40711	Human secreted pro
28	337.5	23.5		1008	24	AAAD30356	Mouse testes-speci
29	318	22.1		3804	21	AACT7617	Human cancer assoc
30	305.5	21.3		882	22	AAST21374	Human cDNA sequenc
31	304.5	21.2		980	21	AAI72857	CDNA clone APPLF.
32	300.5	20.9		429	24	ABL57727	Human sbg1002620T1
33	300	20.9		757	23	AAST0845	DNA encoding novel
34	296.5	20.6		939	22	AAH98659	Rat EST-derived co
35	296.5	20.6		1690	22	AAH15690	Human cDNA sequenc
36	296.5	20.6		1824	24	ABK33563	CDNA encoding huma
37	296.5	20.6		2272	22	AAFT7687	Human prostate-inh
38	296.5	20.6		3836	24	AAH33682	Human secreted pro
39	296.5	20.6		4877	22	AAAS60871	Human cancer agenti
40	296.5	20.6		4877	22	AAAS60883	Human cancer agenti
41	296.5	20.6		4877	22	AAAD01766	Human cancer agenti
42	296	20.6		2403	22	AAAD01766	Human novel trypsi
43	295.5	20.6		1491	22	AAFT7686	Human protease-inh
44	295.5	20.6		1494	24	ABL57728	Human sbg1002620T1
45	295.5	20.6		1669	22	AAAD17765	Human novel trypsi

FT sig-peptide /product- "Human full-length 36PIG3/SGP28 protein"
 FT 3...98 /*tag- b
 FT mat-peptide 99...776 /*tag- c
 FT /product- "Human mature full-length 36PIG3/SGP28 protein"
 FT
 PN WO200131343-A2.
 PD 03-MAY-2001.
 PF 27-OCT-2000: 2000MO-US293607.
 PR 28-OCT-1999: 99US-0162610.
 PA (UROC-) UROGENESYS INC.
 PI Hubert RS, Raitano AB, Afar DEH, Mitchell SC, Faris M;
 PI Jakobovits A;
 DR WPI: 2001-308685/32.
 DR P-PSDB: AAE02211.
 PT Detecting cancers, particularly of prostate and colon, from
 PT overexpression of SGP28 protein, also methods for treating these
 PT cancers e.g. by vaccination with the protein
 PT
 PS Claim 16: Page 62-63; 102pp; English.
 XX
 CC The present invention relates to methods and compositions for the
 CC diagnosis and therapy of prostate cancer which utilise human SGP28
 CC (specific granule protein 28) gene and proteins. The method involves
 CC detecting cancers, particularly of prostate and colon, from
 CC overexpression of SGP28 protein. The expression of SGP28, which is an
 CC extracellular protein is restricted to the prostate and ovary, and is
 CC markedly up-regulated in prostate tumours. SGP28 sequence is used for
 CC diagnosis (including in vivo imaging), staging, monitoring and prognosis
 CC of prostate and colon cancer, and for assisting selection of therapy.
 CC Also SGP28-expressing cancers can be treated by administering a
 CC composition or vaccine that contains a vector expressing an antibody
 CC specific for SGP28 protein, nucleic acid encoding SGP28 protein or its
 CC fragments, polypeptides encoded by SGP28 gene and SGP28-specific antibody
 CC optionally conjugated to toxin or therapeutic agent. SGP28 gene product
 CC is also used as source of therapeutic antisense or ribozyme agents, as
 CC primers/probes for diagnosis or prognosis, to identify compounds that
 CC inhibit calcium entry into prostatic cells, for recombinant production of
 CC SGP28 peptides and for isolating related sequences. SGP28 protein and
 CC its fragments are used to raise specific antibodies (Ab) and to identify
 CC specific binding agents (potentially useful as therapeutic and
 CC diagnostic agents) and also potential anticancer agents. The present
 CC sequence is human full-length 36PIG3/SGP28 cDNA.
 CC
 SQ Sequence 2144 BP; 735 A; 403 C; 382 G; 624 T; 0 other;
 Alignment Scores:
 Pred. No.: 1.8e-136 Length: 2144
 Score: 1436.00 Matches: 258
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-698-781-3 (1-258) x AAD06222 (1-2144)
 QY 1 MetysglnileuHISProAlaLeuGIuThrThraIamethrLeuPheProValIeu 20
 DB 3 ATGAACAACAACTTCACTCCCTCGTGAACACACTGCAATGATATTATTCACAGTCTG 62
 QY 21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
 DB 63 TTGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 122
 QY 41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60

DB 123 TTTACTGCTTTGTTTACCACCCCAACACAACTGCMAAGGGGATGTGAAATMACACAAAT 182
 QY 61 GluLeuArgArgAlaValAsnSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
 DB 183 GAACTGAGAGAGACAGATATCTCCCTGCGCAGAAACATGCTGAAGATGGAATGGACAA 242
 QY 81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrrArgHisSerAsnPro 100
 DB 243 GAGCTGAGCAAAATGCGCAAAAGTGGCAAAACAGTGCATTTACAGACACAGTAACCA 302
 QY 101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrrMetSerSerAlaProSer 120
 DB 303 AAGATGCAATGACAAAGCTTMAATGTGTGAGATCTCTCAATGTCAGTCAAGTCCCGCAGC 362
 QY 121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrrAsnAspPheAspPheGlyVal 140
 DB 363 TCATGGTCACAAAGCAATCCAAAGCTGGTTGATGATGATCAATGATTTGACTTTGGGTGA 422
 QY 141 GlyProLysThrProAsnAlaValAlaGlyHisTyrrThrGlnValAlaTrpTyrrSerSer 160
 DB 423 GGGCCAAAGACTCCCAACGCGAGTGTGACATTAATACAGAGTGTGTGGTACTCTTCA 482
 QY 161 TyrrLeuValGlyCysGlyAsnAlaTyrrCysProAsnGlnLysValLeuLysTyrrTyrr 180
 DB 483 TACCTCGTGGATGTGMAATGCTTACTGTCATCAATCAAAAGTCTMAAATACTACTAT 542
 QY 181 ValCysGlnTyrrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrrValProTyrrGluGln 200
 DB 543 GTTGGCCAAATATGCTCTGCTGTAATGGCTAATGACTATATGTCCTTAAGAACAA 602
 QY 201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
 DB 603 GGACACACTTGTGCGACAGTGTCCAGATTAACGTGACATGATGATGACCAATGGTTGC 662
 QY 221 LysTyrrGluAspLeuTyrrSerAsnCysLysSerLeuLysLeuThrLeuThCysLysHis 240
 DB 663 AAGTACGAAGATCTCTATAGTAACTGTMAAGTTGAAGTCAACATTAACCTGTAAACAT 722
 QY 241 GluLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyrr 258
 DB 723 CAGTTGGACAGACAGACAGTGCATCGCATCTTCGCAATTTCTTAACACACATTAT 776
 RESULT 2
 ABV24823
 ID ABV24823 standard; cDNA; 1610 BP.
 XX
 AC ABV24823:
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 24814.
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW Pharmacogenomic marker; gene; ss.
 XX Homo sapiens.
 PN WO200160860-A2.
 PD 23-AUG-2001.
 PF 20-FEB-2001: 2001MO-US05171.
 PR 17-FEB-2000: 2000US-183319P.
 PR 16-MAR-2000: 2000US-189862P.
 PR 25-MAY-2000: 2000US-207454P.
 PR 09-JUN-2000: 2000US-211314P.
 PR 18-JUL-2000: 2000US-219007P.
 PR 13-DEC-2000: 2000US-255281P.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PI Schlegel R, Endege WO, Monahan JE;

XX WPI: 2001-662795/76.

XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1: Page 4758-4759; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 1610 BP; 543 A; 292 C; 292 G; 483 T; 0 other;

Alignment Scores:
Pred. No.: 2,45e-136 Length: 1610
Score: 1433.00 Matches: 257
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.61% Mismatches: 0
Query Match: 99.79% Indels: 0
DB: 23 Gaps: 0

US-09-698-781-3 (1-258) x ABV24823 (1-1610)

QY 1 MetTgGlnTleuHSProAlaLeuGluThrThraLamethrLeuProvalleu 20
DB 475 ATGAAACAAATACCTCTGCTGGAACCACTCAATGACATTAATCCAGTCTG 534
QY 21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGlyAspProAla 40
DB 535 TTGTTCTGCTGCTGCTGCTGCTTCCATCTTTCCAGCAATGAATGAATGCCGCT 594
QY 41 PheThraLeuLeuThrThrGlnThrGlnValGlnArgGluLeuValAsnLysHisAsn 60
DB 595 TTACTGCTTTGTTAACCCACCAACAAAGTGCAGAGGAGATTCGAATTAACACAAAT 654
QY 61 GluLeuArgTrgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
DB 655 GAACGTGGAGAGCAGATCTCCCTCCGAGAAACATGCTGAGATGGAATGGAAACAAA 714
QY 81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTrpArgHisSerAsnPro 100
DB 715 GAGGCTCAGCAAAATGCCCAAAAGTGGCAAAACAGTGCATTCACAGACAGTAACCA 774
QY 101 LysAspArgMetTrpSerLeuLysCysGlyGluAsnLeuTrpMetSerSerAlaProSer 120
DB 775 AAGGATGGAATGACAAAGTCTAAATGTGTGAGATCTCTCATGATCAAGTCCCGCAGC 834
QY 121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTrpAsnLysValLeuLysVal 140
DB 835 TCATGCTCACAGCAATCCAAAGCTGTTGATCAGTAACAATGATTTGGACTTGGGTGA 894
QY 141 GlyProLysThrProAsnAlaValAlaGlyHisTrpGlnValAlaTrpTrpSerSer 160
DB 895 GGGCAAAAGACTCCCAACTCAGTGTGACATATACACAGTGTGTTGTTACTCTTCA 954
QY 161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyr 180
DB 955 TACCTCGTGAATGTGAAATGCTACTGTCCTCCCAATCAAAAAGTTCTAAATACTACTAT 1014

QY 181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTrpValProTyrGluGln 200
DB 1015 GTTGGCAATATATGCTCTGCTGTTAATGGCTAAATGACTATATGCTTATGAACAA 1074
QY 201 GlyAlaProCysAlaSerCysProAspAsnCysAspGlyLeuCysTrpAsnGlyCys 220
DB 1075 GGAGCACCTTGTGCTCCAGTTCCAGATMACTGACATGACTATGACCAATGTTGC 1134
QY 221 LysTrpGluAspLeuTrpSerAsnCysLysSerLeuLysLeuThrLeuTrpCysLysHis 240
DB 1135 AAGTACAGAAATCTCTATGTAAGTGTAAAGTTTGAAGCTCACATTAACTGTAAACAT 1194
QY 241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
DB 1195 CAGTGTGTCAGGAGCAAGTTCAGAGGCTCCTGCAATGTTCAAAACACATTTAT 1248

RESULT 3

AAH98651
ID AAH98651 standard; cDNA; 2133 BP.

XX AC AAH98651;

DT 12-OCT-2001 (first entry)

DE Human EST-derived coding sequence SEQ ID NO: 508.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder;

XX biodiversity; gene therapy; nutrition; ss.

OS Homo sapiens.

PN W0200154477-A2.

PD 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02687.

PR 25-JAN-2000; 2000US-0491404.

PR 17-JUL-2000; 2000US-0617746.

PR 03-AUG-2000; 2000US-0631451.

PR 15-SEP-2000; 2000US-0663870.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PI Cao Y, Drmanac RA, Zhang J, Werhman T;

XX WPI: 2001-476164/51.

DR P-PSDB; AAM23992.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising

PT antibodies and research use -

XX Claim 1: Page 533; 1275pp; English.

PS The present invention provides the protein and coding sequences of novel

CC proteins from a variety of organisms, including human, dog, cat, horse,

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

CC urchin and tomato. These were derived from expressed sequence tags (ESTs)

CC from the organism of interest. They can be used in diagnostics,

CC forensics, gene mapping, identification of mutations, to assess

CC biodiversity and for nutritional purposes. The present sequence is a cDNA

CC of the invention.

XX Sequence 2133 BP; 725 A; 403 C; 382 G; 623 T; 0 other;

SO Alignment Scores:
Pred. No.: 1.17e-135 Length: 2133
Score: 1428.00 Matches: 257
Percent Similarity: 99.61% Conservative: 0

Best Local Similarity: 99.61% Mismatches: 1
 Query Match: 99.44% Indels: 0
 DB: 22 Gaps: 0

US-09-698-781-3 (1-258) x AAH98651 (1-2133)

OY 1 MetlysglnileuHlsProAlaLeuGluThrAlaMetThrLeuPheProValleu 20
 DB 2 ATGAACAATACTTCACTGCTGGAACCACTGCAATGACATTAATCCAGTGTG 61
 OY 21 LeupheleuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
 DB 62 TTGTTCCGTGCTGGGCTGCTTCCATCTTTCCAGCAATGAAGATGAAGATCCGCT 121
 OY 41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
 DB 122 TTTACTGCTTGTATACCAACCAACCAAGCAAGATGTAATGAATGAACCAAT 181
 OY 61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
 DB 182 GAAGTGAAGAGAGAGATATCTCCCTCCAGAAACATGCTGAATGGAATGAACAA 241
 OY 81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyArgHisSerAsnPro 100
 DB 242 GAGCTGCAGCAAAATGCCCAAAAGTGCGCAACAGTCAATTAACAGACAGTAACCA 301
 OY 101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyMetSerSerAlaProSer 120
 DB 302 AAGATTCACATGACAAAGCTTAAATGTGTGATCTCTACATGTCAAGTCCCTCAGC 361
 OY 121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyTrpAsnAspPheAspHelyAl 140
 DB 362 TCATGTGTACAAAGCAATCCAAAGCTGTGTGATGAGTCAATGATTTGACTTGTGTA 421
 OY 141 GlyProLysThrProAsnAlaValAlaGlnLysTyTrpGlnValAlaTrpTrpSerSer 160
 DB 422 GGGCCAAAGATCCCAACAGAGTGTGTGACATTATACAGAGTGTGTGTGACTTCA 481
 OY 161 TyrLeuValAlaGlyCysGlyAsnAlaTyrcysProAsnGlnLysValLeuLysTyTrp 180
 DB 482 TACCTCGTGTGATGTGAAATGCCCTACCTGCCAATCAAAAGTCTAAATACACTAT 541
 OY 181 ValCysGlnTyrcysProAlaGlyAsnTrpAlaAsnArgLeuTyValProTyrcyluGln 200
 DB 542 GTTGTCCAAATGTGCTGCTGTGATGCTAATGAGTATGATGCTCCCTTATACAA 601
 OY 201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
 DB 602 GGAGCACTTGTGGCCAGTTGCCAGATAGCTGTGACATGACATGCAACCAATGCTGC 661
 OY 221 LysTrpGluAspLeuTyrcysAsnCysLysSerLeuLysLeuThrLeuThrcysLysHis 240
 DB 662 AAGTACGAGAGATCTCTATAGTAACTGTAAGTTGAAGCTCACATTAACCTGTAACAT 721
 OY 241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyrc 258
 DB 722 CAGTTGTGAGGAGACAGTTGCAAGGCAATCTGCAATTTGTTCAACAGCATTTAT 775

RESULT 4
 AAH98659 standard: cDNA: 2133 BP.
 AAH98659:
 12-OCT-2001 (first entry)
 Human EST-derived coding sequence SEQ ID NO: 516.
 Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 diagnostics; forensic test; gene mapping; genetic disorder;
 biodiversity; gene therapy; nutrition; ss.

OS Homo sapiens.
 XX WO200154477-A2.
 XX 02-AUG-2001.
 PD 25-JAN-2001; 2001WO-US02687.
 PF 25-JAN-2001; 2000US-0491404.
 XX 25-JAN-2000; 2000US-0617746.
 PR 17-JUL-2000; 2000US-0617746.
 PR 03-AUG-2000; 2000US-0631451.
 PR 15-SEP-2000; 2000US-0663870.
 XX (HXSE-) HXSEQ INC.
 PA Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
 PI Cao Y, Drmanac RA, Zhang J, Wehrman T;
 XX WPI: 2001-476164/51.
 DR P-PSDB: AAM24000.
 XX Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use -
 PS Claim 1: Page 537-538; 1275pp: English.
 XX The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA
 CC of the invention.
 SQ Sequence 2133 BP; 725 A; 403 C; 382 G; 623 T; 0 other:
 Alignment Scores:
 Pred. No.: 1,17e-135 Length: 2133
 Score: 1428.00 Matches: 257
 Percent Similarity: 99.61% Conservative: 0
 Best Local Similarity: 99.61% Mismatches: 1
 Query Match: 99.44% Indels: 0
 DB: 22 Gaps: 0

US-09-698-781-3 (1-258) x AAH98659 (1-2133)

OY 1 MetlysglnileuHlsProAlaLeuGluThrAlaMetThrLeuPheProValleu 20
 DB 2 ATGAACAATACTTCACTGCTGGAACCACTGCAATGACATTAATCCAGTGTG 61
 OY 21 LeupheleuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
 DB 62 TTGTTCCGTGCTGGGCTGCTTCCATCTTTCCAGCAATGAAGATGAAGATCCGCT 121
 OY 41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
 DB 122 TTTACTGCTTGTATACCAACCAACCAAGCAAGATGTAATGAATGAACCAAT 181
 OY 61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
 DB 182 GAAGTGAAGAGAGAGATATCTCCCTCCAGAAACATGCTGAATGGAATGAACAA 241
 OY 81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyArgHisSerAsnPro 100
 DB 242 GAGCTGCAGCAAAATGCCCAAAAGTGCGCAACAGTCAATTAACAGACAGTAACCA 301
 OY 101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyMetSerSerAlaProSer 120
 DB 302 AAGATTCACATGACAAAGCTTAAATGTGTGATCTCTACATGTCAAGTCCCTCAGC 361
 OY 121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyTrpAsnAspPheAspHelyAl 140

DB 362 TCATGCTCACAAAGCAATCCAAAGCTGTTGATGAGTACATGATTTTGACTTGGTGA 421
OY 141 GYProLYsThrProAsnAlaValAlGlyHisTyrThGlnValAlaTTPYrSerSer 160
DB 422 GGGCCAAAGATCCCAACGAGTGGTGGACATTATACACAGGTGGTGGTACTCTTCA 481
OY 161 TYLeuValAlGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyr 180
DB 482 TACCTGCTGGATGTGGAAATGCTTACTGTCCCAATCAAAAAGTTCTAAATACTACTAT 541
OY 181 ValCysGlnTyrCysProAlaGlyAsnTyrPalaAsnArgLeuTyrValProTyrGluGln 200
DB 542 GTTGGCAATATGTCTGCTGCTGTAATGGCTAATAGACTATATGCTTATGAAACAA 601
OY 201 GYAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
DB 602 GGAGCAGCTTGTCCAGTTGCCAGATTAAGTGCAGCATGAGTATGACCAATGGTTC 661
OY 221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
DB 662 AAGTACGAGATCTCTATTAAGTAAAGTTGAAGCTCACATTAACTGTAACAT 721
OY 241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
DB 722 CAGTTGGTCAGGAGCAGTTGCCAAGCATCTGCAATGTTCAAACACACATTAT 775
RESULT 5
ABV22644
ID ABV22644 standard; cDNA; 2452 BP.
AC ABV22644;
XX
XX 13-SEP-2002 (first entry)
DE Human prostate expression marker cDNA 22635.
XX
XX Human prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene: ss.
XX
XX Homo sapiens.
OS
XX
XX WO200160860-A2.
PN
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX
PI Schlegel R, Endege WO, Monahan JE.
XX
XX WPI; 2001-662795/76.
DR
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 3969-3970; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;

CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
XX Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 1,43e-135 Length: 2452
Score: 1428.00 Matches: 257
Percent Similarity: 99.61% Conservative: 0
Best Local Similarity: 99.61% Mismatches: 1
Query Match: 99.44% Indels: 0
DB: 23 Gaps: 0
US-09-698-781-3 (1-258) x ABV22644 (1-2452)
OY 1 MetLysGlnIleLeuHisProAlaLeuGluThrThAlaMetThrLeuPheProValLeu 20
DB 197 ATGAACAAATACTTCTATCTGCTGGAAACACACTGCAATGACATTATCCCAAGTCTG 256
OY 21 LeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
DB 257 TTGTTCTGTTGCTGGGCTGCTGCTTCATCTTCCACCAATGAAGTAAAGATCCCGCT 316
OY 41 PheThrAlaLeuLeuThrThrGlnThrGlnValAlaArgGluLeuValaLysHisAsn 60
DB 317 TTTACTGCTTTGTTAAACACCAACCAAGTGCAGAAAGGAGATGGAATTAAGCACAAAT 376
OY 61 GlnLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTPAsnLys 80
DB 377 GAACCTGAGAGACAGATATCTCCCTGCCAGAAACATGCTGAAGATGAAGTGAACAAA 436
OY 81 GlnAlaAlaAlaAsnAlaGlnLysTyrPalaAsnGlnCysAsnTyrArgHisSerAsnPro 100
DB 437 GAGGCTGCACCAATGCCCCAAAGTGGCAACAGTGCATTTACACACACAGTAAACCA 496
OY 101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
DB 497 AAGGATGGAATGACAAATCTTAAATGTGTGAGATCTTAACATGCAAGTCCACAGC 556
OY 121 SerTyrSerGlnAlaAlaGlnSerTyrPheAspGluTyrAsnAspPheAspGlyVal 140
DB 557 TCATGCTCACAAAGCAATCCAAAGCTGTTGATGATGATGATGATTTTGAATTTGCTGTA 616
OY 141 GYProLYsThrProAsnAlaValAlGlyHisTyrThrGlnValAlaTTPYrSerSer 160
DB 617 GGGCCAAAGACTCCCAACGAGTGGTGGACATTATACACAGGTGGTGGTACTCTTCA 676
OY 161 TYLeuValAlGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyr 180
DB 677 TACCTGCTGGATGTGGAAATGCTTACTGTCCCAATCAAAAAGTTCTAAATACTACTAT 736
OY 181 ValCysGlnTyrCysProAlaGlyAsnTyrPalaAsnArgLeuTyrValProTyrGluGln 200
DB 737 GTTGGCAATATGTCTGCTGCTGTAATGGCTAATAGACTATATGCTTATGAAACAA 796
OY 201 GYAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
DB 797 GGAGCAGCTTGTCCAGTTGCCAGATTAAGTGCAGCATGAGTATGACCAATGGTTC 856
OY 221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis 240
DB 857 AAGTACGAGATCTCTATTAAGTAAAGTTGAAGCTCACATTAACTGTAACAT 916
OY 241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
DB 917 CAGTTGGTCAGGAGCAGTTGCCAAGCATCTGCAATGTTCAAACACACATTAT 970

RESULT 6
 ABV24631
 ID ABV24631 standard; cDNA: 2452 BP.
 XX
 AC ABV24631;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 24622.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI: 2001-662795/76.
 XX
 PT Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer -
 XX
 PS Claim 1; Page 4680-4681; 11750pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
 CC
 CC Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;
 XX
 SQ
 Alignment Scores:
 Pred. No: 1,43e-135 Length: 2452
 Score: 1428.00 Matches: 257
 Percent Similarity: 99.61% Conservative: 0
 Best Local Similarity: 99.61% Mismatches: 1
 Query Match: 99.44% Indels: 0
 DB: 23 Gaps: 0
 US-09-698-781-3 (1-258) x ABV24631 (1-2452)
 OY 1 MetygslnleuHlspRoalaLeuGluThrAlaMetThrLeuPheProValleu 20
 DB 197 ATGAAGAAATACTTCTTCCTGCGAAACCACTGCAATGACATTAATCCAGTCTG 256
 OY 21 LeupheValaIaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40

DB 257 TTTCTTCCTGGTCTGCTGGCGCTTCCATCTTTTCCAGCAATGAAATAGATCCCGCT 316
 OY 41 PheThrAlaLeuLeuThrThrGlnThrGlnValAlaArgGluLeuValAsnLysHsAsn 60
 DB 317 TTACTGCTTTGTTAAACCAACCAACCAAGCAAGTGTGTAATAGCAACAT 376
 OY 61 GluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTrpAsnLys 80
 DB 377 GAACGTAGAGAGACAGTATCTCCCTCCAGAAACATGCTGAAAGATGAAAGCAAA 436
 OY 81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTrpArgHsSerAsnPro 100
 DB 437 GAGCTCAGCAAAATGCCAAAGTGGCAACCAATGCAATTAACAGACAGTAACCA 496
 OY 101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerAlaProSer 120
 DB 497 AAGGATCGAATGACAAAGTCTAAATGTGTGAAATCTTACTGTCAAGTCTCCAGC 556
 OY 121 SerTrpSerGlnAlaAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspHeglyVal 140
 DB 557 TCATGGTCACAAGCAATCCAAAGCTGTTGATGAGTACAAATGATTTGACTTGGTGA 616
 OY 141 GlyProLysThrProAsnAlaValAlaGlyHsTrpThrGlnValAlaTrpTyrSerSer 160
 DB 617 GGCCCAAGACTCCCAACCCAGTGTGGACATTAACACAGGTGTTGGTACTCTTCA 676
 OY 161 TyrLeuValAlaGlyCysGlyAsnAlaTyrCysProAsnGluValLeuLysTrpTyr 180
 DB 677 TACCTCGTTGATGTGGAATCCCTACTCTCCCAATCAAAAGTCTTAATAACTACTAT 736
 OY 181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln 200
 DB 737 GTTCCCAATATTGTCTGCTGCTGTAATGGCTAATAGACTATATGCTCCCTATACAA 796
 OY 201 GlnAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys 220
 DB 797 GGAGCACTGTGTGCCAGTGTGCCAATATCTGTGACATGGAGTATGCCCAATGTGTGC 856
 OY 221 LysTyrGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrCysLysHs 240
 DB 857 AAGTACGAAGACTCTATAGTACTGTAAAGCTTGAAGCTACATTAACCTGTAACAT 916
 OY 241 GlnLeuValAlaArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
 DB 917 CAGTTGGTCAGGAGACAGTTGCCAAGGCTCTGCAATGTGTCAAAACAGCATTTAT 970
 RESULT 7
 ID ABV25272 standard; cDNA: 2452 BP.
 XX
 AC ABV25272;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 25263.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.

DB 61 / GGGCAAGACGCCCAACGCAGTGGTGGACATATACACAGGTGGTGGTACCTTCA 6 /

CC (f) assessing the prostate cell carcinogenic potential of a compound;

CC (g) determining whether prostate cancer has metastasized in a patient;

CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
 XX
 SQ Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;

Alignment Scores:

Pred. No.:	1,436-135	Length:	2452
Score:	1428.00	Matches:	257
Percent Similarity:	99.61%	Conservative:	0
Best Local Similarity:	99.61%	Mismatches:	1
Query Match:	99.44%	Indels:	0
DB:	23	Gaps:	0

US-09-698-781-3 (1-258) x ABV25706 (1-2452)

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OY 1 MettysGlnlleuHisProAlaLeuGluThrThraAlaMetThrleuPheProValleu 20
DB 197 ATGAACAATAATCTTCACTCTGCTGGAACCACTGCATGACATATATCCAGTGTG 256
OY 21 LeupheleuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
DB 257 TTGTTCCGTGCTGCTGCTGCTTCCATCTTTCCAGCAATGAAGATAGATCCGCT 316
OY 41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
DB 317 TTTACTGCTTTGTAAACCAACCAACACAAAGCAAGGAGATGTGAATAGACACAT 376
OY 61 GlutAspArgAlaValSerProProAlaArgAsnMetLeuLysMetCyluTrpAsnLys 80
DB 377 GAACGAGAGAGAGCAATCTCTCCCTGCGAAGAACATCTTAAGATGGAAGAACAA 436
OY 81 GluAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTyrArgHisSerAsnPro 100
DB 437 GAGCGTGACGAATATGCCAAAGTGGGCAACCAAGTGCATTAACAGACAGTAACCA 496
OY 101 LysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTyrMetSerSerAlaProSer 120
DB 497 AAGGATCGAATGACAAAGCTTAAATGTGTGAAATCTCTACATGTCAAGTCCCTCAGC 556
OY 121 SerTPSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspHeGlyVal 140
DB 557 TCATGCTCACAAGCAATCCAAAGCTGTTGTGATGATACATGATTTTGTGCTGA 616
OY 141 GlyProLysThrProAsnAlaValAlaGlyHisTyrThrGlnValAlaTrpTyrSerSer 160
DB 617 GGGCCAAAGACTCCCAACGACTGTTGACATATACACAGTGTGTTGTAACCTTCA 676
OY 161 TyrLeuValAlaGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyr 180
DB 677 TACCTCGTTGATGTGGAATGCCACTGTCCCAATCAAAAGTCTTAAATAACACTAT 736
OY 181 ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGlnGln 200
DB 737 GTTTCACATATATGCTCTGCTGTAATGGCTAATAGACTATATGCTTATGACAA 796
OY 201 GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuLysThrAsnGlyCys 220
DB 797 GGAGACCTTGTGCGAGTGGCCACATTAATCTGACGATGAGTATGACCAATGTTGCT 856
OY 221 LysTyrGluAspLeuTyrSerAsnLysSerLysSerLysLeuThrLeuThrCysLysHis 240
DB 857 AAGTACGAAGATCTTATATGTAAGTAAAGTTTGAAGCTCATTAACTGTAACAT 916
OY 241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr 258
DB 917 CAGTTGGTCAGGAGACATTGCAAGGCTCTCTCATTTGTTCAACAGCATTTAT 970

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RESULT 9
 ABV28467
 ID ABV28467 standard; cDNA: 2452 BP.
 XX
 AC ABV28467;

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XX 16-SEP-2002 (first entry)
DT
XX
XX Human prostate expression marker cDNA 28458.
DE
XX
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
KM
XX Homo sapiens.
OS
XX WO200106860-A2.
PN
XX
XX
PD
XX
XX 23-AUG-2001.
XX
XX 20-FEB-2001; 2001WO-US05171.
XX
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI
XX
XX Schlegel R, Endege WO, Monahan JE;
XX
XX WPI: 2001-662795/76.
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
XX Claim 1; Page 5942-5943; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.
SQ
XX
XX Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 1,436-135 Length: 2452
XX Score: 1428.00 Matches: 257
XX Percent Similarity: 99.61% Conservative: 0
XX Best Local Similarity: 99.61% Mismatches: 1
XX Query Match: 99.44% Indels: 0
XX DB: 23 Gaps: 0
XX
XX US-09-698-781-3 (1-258) x ABV28467 (1-2452)
OY 1 MettysGlnlleuHisProAlaLeuGluThrThraAlaMetThrleuPheProValleu 20
DB 197 ATGAACAATAATCTTCACTCTGCTGGAACCACTGCATGACATATATCCAGTGTG 256
OY 21 LeupheleuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
DB 257 TTGTTCCGTGCTGCTGCTGCTTCCATCTTTCCAGCAATGAAGATAGATCCGCT 316
OY 41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60

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Db	317	TTTTCTGCTTTGTTAAACCCACCCAAACCAACGATGCAAAAGGACGATGTGTAATAAGCAACAT	376
Qy	61	GluleuAArgAlaValSerProFcoliaAArgAsnMetLeuLysMetGluTrpAsnLys	80
Db	377	GAATGAGAGAGACGATATCTCCCTCGCCAGAAACATGCTGAAGATGGAATGGAACAAA	436
Qy	81	GlulAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTrpArgHisSerAsnPro	100
Db	437	GAGGCTCAGCAAAATGCCCAAAAGTGGGCAAAACAGGCAATTACAGACACAGTAACCCA	496
Qy	101	LysAspArgMetThrSerLeuLysCysGlgLysAsnLeuLysMetSerSerAlaProSer	120
Db	497	AAGATTCGAATGACAACTCTAATAATGTCGTGACAAATCTTCACTATGTCMACTGCCCTCAGC	556
Qy	121	SerTrpSerGlnAlaAlaGlnSerTrpPheAspGluTrpAsnAspPheAspPheGlyVal	140
Db	557	TCATGAGTCACAAACATCCAAAGCTGGTTGATGACGACATATATTTTGACTTTGGTGA	616
Qy	141	GlyProLysThrProAsnAlaValAlaGlnHisTrpThrGlnAlaValTrpTrpSerSer	160
Db	617	GGGCGCAAGACTCCCAAGCGAGTGTGTGACATTAATACACAGGTTGTTGTGACTCTCA	676
Qy	161	TyrLeuValGlyCysGlyAsnAlaLysCysProAsnGlnLysValLeuLysTyrTyr	180
Db	677	TACCGCGTGGATGTGGAAATGCTACTGTGCCAATCAAAAAGTCTAATAATACTACTAT	736
Qy	181	ValCysGlnTyrCysProAlaGlyAsnTrpAlaAsnArgLeuTyrValProTyrGluGln	200
Db	737	GTTTGCCCAATATGTCTCGCTGCTGAATGGGCTATATGACTATATATGCCCTTATGAACAA	796
Qy	201	GlyAlaProCysAlaSerCysProAspAsnCysAspAspGlyLeuCysThrAsnGlyCys	220
Db	797	GGAGACCTTGTGCGAGTGGCCCGCATTAAGTACGATGACATGAGACTATGACCAATGGTTGC	856
Qy	221	LysTrpGluAspLeuTyrSerAsnCysLysSerLeuLysLeuThrLeuThrCysLysHis	240
Db	857	AAGTACGAAGATCTCTAATAGTAACTGTAAAGTTTGAAGCTCACATTAATACCTGTAAACAT	916
Qy	241	GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyr	258
Db	917	CAGTTGCGTACAGGACAGTTCGCAAGGCTCGTCAATATGTTCAACACAGCAATTAAT	970
RESULT 10			
ABV28648	ID	ABV28648 standard; cDNA: 2452 BP.	
XX	AC	ABV28648;	
XX	DT	16-SEP-2002 (first entry)	
XX	DE	Human prostate expression marker cDNA 28639.	
XX	KW	Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker; pharmacogenomic marker; gene; ss.	
XX	OS	Homo sapiens.	
XX	PN	WO200160860-A2.	
XX	PD	23-AUG-2001.	
XX	PF	20-FEB-2001; 2001WO-US05171.	
XX	PR	17-FEB-2000; 2000US-183319P.	
XX	PR	16-MAR-2000; 2000US-189863P.	
XX	PR	25-MAY-2000; 2000US-207454P.	
XX	PR	09-JUN-2000; 2000US-211314P.	
XX	PR	18-JUL-2000; 2000US-219007P.	
XX	PR	13-DEC-2000; 2000US-255281P.	
XX	PA	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
XX	PI	Schlegel R, Endege WO, Monahan JE;	

WPI; 2001-662795/76.

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -

Claim 1; Page 6006; 11750pp; English

CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV000010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 2452 BP; 787 A; 467 C; 444 G; 754 T; 0 other;

Alignment Scores:

Pred. No.:	1.43e-135	Length:	2
Score:	1428.00	Matches:	2

Best Local 5

DB: 23

US-09-698-781-3 (1-258) x ABV28648 (1-2452)

QY 1 MettysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuPheProValLeu 20

Db 197 ATGAACAATACTTCATCCTGCTCTGGAACCACTGCAATGACATTATCCAGTCTG 255

QY. 21 LeupheLeuValAlaGlyLeuLeuProSerPhePheProAlaAsnGluAspLysAspProAla 40

Db 257 TTGTTCCCTGGTTGCTGGGCTGCTTCCATCTTTTCCAGCAATGAAGATAGGATCCCGCT 31

QY 41 pHeThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 600

Db 317 TTTACTGCTTTGTTAACCCACCAACACAGTGCACAAGGAGATTGTGAATAAGCACAAT 37

QY 61 GIULEuARgAlaValSerPRoPRoAlaARgASmetLeuLysmetGIUTPRAsnLys 80

Db 377 GAACTGAGGAGAGCAGTATCTCCCCCTGCCAGAAACATGCTGAGATGGAATGGAACCAA 433

QY 81 GIUAIAAIAAsnAAGlnLysTRPALAAsnGlnCysAsnTYRArgHisSerAsnPro 100

Db 437 GAGGCTGCAGCAATGCCCAAGTGGCAACCCAGTGCATTACAGACACAGTAACCA 499

QY 101 Lysaspargmethrserleulyscysglygluasnleutyrmetserseralaproser 12

Db 497 AAGGATCGATGACCAAGTCTAAATGTGGTGAGAACTCTACATGTCACAGTGCCCTCCAGC 55

QY 121 SerTrpSerGlnAlaIleGlnSerTrpPheAspGluTyrAsnAspPheAspPheGlyVal 14

Db 557 TCATGGTCACAGCAATCCAAAGCTGGTTGATGAGTACACATGATTTGACTTTGGTGA 611

141 GIVPROLVSThrPROASNAIaValValGlyHISTYrThrcInValValTrpTYrSerSer 16

Db 617 GGGCCAAGACTCCCAACGCGAGTGGTTGGACATTATACACAGGTTGTTGGTACTCTTCA 67

QY 161 TyrLeuValGlyCysGlyAsnAlaTyrCysProAsnGlnLysValLeuLysTyrTyrTyr 18

Db 677 TACCTCGTGGATGTGGAATGCCCTACTGTCCCAATCAAAAAGTTCTAAAATACTACTAT 733

OY 181 ValysgIntRyCysPrioAlaGlyAsnTrpAlaAsnArgLeuTyValProTyGluGln 200
 DB 737 GTTGGCCAAATATTGCTCCGTGCTATGAGGCTATAGACTATATGCTCCATATGACAA 796
 OY 201 GllvAlaProCysAlaSerCysPrioAspAspAspGlyLeuCysThrAsnGlyCys 220
 DB 797 GGAGCACCCTTGTCCAGTGTGCCAGATACGTGTGACGATGATGACCAATGGTTGC 856
 OY 221 LysTyGlnAspLeuTySerAsnCysLysSerLeuTyLeuThrLeuThrCysLysHis 240
 DB 857 AAGTACGAAAGATCTCTATAGTAAAGTTGAAAGCTCAGCTTAACCTTAACAT 916
 OY 241 GlnLeuValArgAspSerCysLysAlaSerCysAsnCysSerAsnSerIleTyR 258
 DB 917 CAGTTGGTCAGGACGACAGTTCAGAGCCCTCTGCAATTGTCACCAACAGCATTTAT 970
 RESULT 11
 ABL67806
 ID ABL67806 standard; DNA; 2128 bp.
 XX
 AC ABL67806;
 XX
 DT 15-MAY-2002 (first entry)
 XX
 DE Oesophagus cancer related gene sequence SEQ ID NO:6143.
 XX
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytosaratic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200194629-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 30-MAY-2001; 2001MO-US10838.
 XX
 PR 05-JUN-2000; 2000US-209473P.
 PR 05-JUN-2000; 2000US-209531P.
 PR 18-SEP-2000; 2000US-231133P.
 PR 18-SEP-2000; 2000US-233617P.
 PR 20-SEP-2000; 2000US-234009P.
 PR 20-SEP-2000; 2000US-234034P.
 PR 20-SEP-2000; 2000US-234052P.
 PR 22-SEP-2000; 2000US-234509P.
 PR 22-SEP-2000; 2000US-234567P.
 PR 25-SEP-2000; 2000US-234923P.
 PR 25-SEP-2000; 2000US-234924P.
 PR 25-SEP-2000; 2000US-235077P.
 PR 25-SEP-2000; 2000US-235082P.
 PR 25-SEP-2000; 2000US-235134P.
 PR 25-SEP-2000; 2000US-235280P.
 PR 26-SEP-2000; 2000US-235637P.
 PR 26-SEP-2000; 2000US-235638P.
 PR 27-SEP-2000; 2000US-235711P.
 PR 27-SEP-2000; 2000US-235720P.
 PR 27-SEP-2000; 2000US-235840P.
 PR 27-SEP-2000; 2000US-235863P.
 PR 28-SEP-2000; 2000US-236028P.
 PR 28-SEP-2000; 2000US-236032P.
 PR 28-SEP-2000; 2000US-236033P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236034P.
 PR 28-SEP-2000; 2000US-236109P.
 PR 28-SEP-2000; 2000US-236111P.
 PR 29-SEP-2000; 2000US-236842P.
 PR 29-SEP-2000; 2000US-236891P.
 PR 02-OCT-2000; 2000US-237172P.
 PR 02-OCT-2000; 2000US-237173P.
 PR 02-OCT-2000; 2000US-237278P.
 PR 02-OCT-2000; 2000US-237294P.
 PR 02-OCT-2000; 2000US-237295P.
 PR 02-OCT-2000; 2000US-237295P.

PR 02-OCT-2000; 2000US-237316P.
 PR 03-OCT-2000; 2000US-237425P.
 PR 03-OCT-2000; 2000US-237598P.
 PR 03-OCT-2000; 2000US-237604P.
 PR 03-OCT-2000; 2000US-237606P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 03-OCT-2000; 2000US-237608P.
 PR 01-NOV-2000; 2000US-244867P.
 PR 01-NOV-2000; 2000US-245084P.
 XX
 PA (AVAL-) AVALON PHARM.
 XX
 PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
 PI Soppet DR, Weaver Z;
 XX
 DR WPI: 2002-188264/24.
 XX
 PT Screening for anti-neoplastic agent involves exposing cells to a
 PT chemical agent to be tested for anti-neoplastic activity, and
 PT determining a change in expression of a gene of a signature gene set
 XX
 PS Claim 1; SEQ ID 6143; 44pp; English.
 XX
 CC The present invention describes a method (M1) for screening for an
 CC anti-neoplastic agent. The method involves exposing cells to a chemical
 CC agent to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (1) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening
 CC an anti-neoplastic agent, and can be used for producing a product which
 CC is the data collected with respect to the anti-neoplastic agent as a
 CC result of M1, and the data is sufficient to convey the chemical
 CC structure and/or properties of the agent. M1 can be used in the
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,
 CC oesophagal, ovarian, kidney, prostate or pancreatic cancer,
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine
 CC carcinoma, papillary carcinoma and Wilm's tumour.
 CC
 SQ Sequence 2128 bp; 734 A; 397 C; 380 G; 617 T; 0 other;
 Alignment Scores:
 Pred. No.: 2.26e-131 Length: 2128
 Score: 1386.00 Matches: 249
 Percent Similarity: 99.60% Conservative: 0
 Best Local Similarity: 99.60% Mismatches: 1
 Query Match: 96.52% Indels: 0
 DB: 24 Gaps: 0
 US-09-698-781-3 (1-258) x ABL67806 (1-2128)
 OY 9 LeuGluTrpThrAlaMetThrLeuPheProValLeuLeuValAlaGlyLeuLeu 28
 DB 1 CTGGAAACCTGCAATGACATTAATTCACAGTGTGTTGCTGGTGGCTGCTCTT 60
 OY 29 ProSerPheProAlaAsnGluAspLysAspProAlaPheThrAlaLeuLeuThrGln 48
 DB 61 CCATCTTTCCAGCAAAATGAAGATAGAGATCCCGCTTTTACTGTTGTTTACACCCAA 120
 OY 49 ThrGlnValGlnArgGluIleValAlaAsnLysHisAsnGluLeuArgAlaValSerPro 68
 DB 121 ACACAGTGCAGAAAGGAGATTGTAATGACATGACATGACAGAGAGAGCATCTCC 180
 OY 69 ProAlaArgAsnMetLeuLysMetGluTrpAsnLysGluAlaAlaAsnAlaGlnLys 88
 DB 181 CCTGCCGAAACATGCTGAAATGAAATGAAAGAGGCTGACGCAAAAGCCCAAAAG 240
 OY 89 TrpAlaAsnGlnCysAsnTyraArgHisSerAsnProLysAspArgMetThrSerLeuLys 108
 DB 241 TGGCAAAACGATGCAATTACAGACAGTAAACCAAGATGCAATGACAAAGTCTAAA 300
 OY 109 CysGlyGluAsnLeuTyMetSerSerAlaProSerSerTrpSerGlnAlaIleGlnSer 128

```

Db 301 TGTGGGAGAAATCTACTGTAAGTGGCTCCAGCTACTGTCACAGCAATCCAAAGC 360
Oy 129 TTPPheaspGluTyrasnAspPheaspPheGlyValGlyProLysThrProAsnAlaVal 148
Db 361 TGGTTGATGAGTACAAATGATTTGACTTGTGGTAGGGCCAAAGACTCCCAACGAGTG 420
Oy 149 ValGlyHisTyrThrGlnValValTrrPyrSerSerTyrLeuValGlyCysGlyAsnAla 168
Db 421 GTTGGACATTATACACAGGTGTTGGTACTCTTCATACCTCGTGGAGTGGAAATGCC 480
Oy 169 TYRCysProAsnGlnLysValLeuLysTyrTyrTyrValCysGlnTyrCysProAlaGly 188
Db 481 TACTGTCACCAATCAAAAGTCTTAAATCTACTATGTTGGCAATATTTGCTGCGGT 540
Oy 189 AsnTrrPalaAsnArgLeuTyrValProTyrGluGlnGlyAlaProCysAlaSerCysPro 208
Db 541 AATTGGGCTAATAGACTATATGTCCCTTATGAAACAAGAGACACTTGTGCGAGTGGCCA 600
Oy 209 AspAsnCysAspAspGlyLeuCysThrAsnGlyCysLysTyrGluAspLeuTyrSerAsn 228
Db 601 GATTAAGTGTGACATGACATGACATGACCAATGTTGCAAGTACGAAAGATCTTATAGTAC 660
Oy 229 CysLysSerLeuLysLeuThrLeuThrCysLysHisGlnLeuValArgAspSerCysLys 248
Db 661 TGTAAAGTTTGAAGCTCACATTAACCTGTAAACATCATGTTGGTAGGAGAGTTCGCAAG 720
Oy 249 AlaSerCysAsnCysSerAsnSerIleTyr 258
Db 721 GCCTCGCTGCAATTTGTTCAACAGACATTTAT 750

RESULT 12
AAS70843 standard; cDNA; 1386 BP.
AAS70843;
XX
AC AAS70843;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #6647.
XX
KM Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS Homo sapiens.
XX
PN MO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001MO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
XX
DR P-PSDB: ABG06656.
XX
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
PS Claim 1: SEQ ID NO 6647; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The

```

```

CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1386 BP; 438 A; 293 C; 289 G; 366 T; 0 other;
Alignment Scores:
Pred. No.: 1,94e-92 Length: 1386
Score: 1002.00 Matches: 184
Percent Similarity: 80.84% Conservative: 27
Best Local Similarity: 70.50% Mismatches: 45
Query Match: 69.78% Indels: 5
DB: 23 Gaps: 3
US-09-698-781-3 (1-258) x AAS70843 (1-1386)
Oy 1 MetLysGlnLeuHisProAlaLeuGluThr-Thr-----AlaMetThrLeuPhepr 18
Db 195 ATTAAGTAGATATTTCATCTCTGCTCAGAAAACCAACATTTCACAGCAATGGCTTACTAC 254
Oy 18 OValLeuLeuPheLeuValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLys 38
Db 255 GGTG---TTGTTCTGGTTACTGTCGTGCTCCATCTTACTCTCA--GAAAGAAAGGA 308
Oy 38 ProAlaPheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluLeuValAsnLys 58
Db 309 TCCCGCTTTTACTGCTTGTGTTAACCCACCAGTCCAGTGAAGGAGGAGATTGTAATAA 368
Oy 58 SHLAsnGluLeuArgArgAlaValSerProProAlaArgAsnMetLeuLysMetGluTr 78
Db 369 ACACAAATGAACCTAAGGAAGAGAGTCTCTCCACTGCCAGTAACTGCTAAAGATGGAA 428
Oy 78 PAsnLysGluAlaAlaAlaAsnAlaGlnLysTrrPalaAsnGlnCysAsnTyrArgHis 98
Db 429 GAGCAGAGAGGTATACACGAATGCCCAAGAGTGGCAAAAGTCAACTTACCAACATAG 488
Oy 98 rAsnProLysAspArgMetThrSerLeuLysCysGlyGlnAsnLeuTyrMetSerSerAl 118
Db 489 TGATCCAGAGAGCAGCAAAACAGTACAGATGAGTGAATCTTATATGCAAGTGA 548
Oy 118 aProSerSerTrrPheSerGlnAlaIleGlnSerTrrPheaspGluTyrAsnAspPheaspPh 138
Db 549 CCTACTTCTCGTCTTCTGCAATCCAAAGCTGGTATGACAGATCCAGATTTGTGCTA 608
Oy 138 eGlyValGlyProLysThrProAsnAlaValAlaGlyHisTyrThrGlnValValTrrPty 158
Db 609 TGTGTAGAGACCAAAAGATCCCAATGCGTGTGGACATATATCTACGCTTGTGGTA 668
Oy 158 rSerSerTyrLeuValGlyCysGlyAsnAlaIleTyrCysProAsnGlnLysValLeuLysTyr 178
Db 669 CTCGACTTACAGGATAGGCTGTGAATTTGCTACTGCTCCATCAAGTACTCTAAATA 728
Oy 178 rTrrTyrValCysGlnTyrCysProAlaGlyAsnTrrPalaAsnArgLeuTyrValProTy 198
Db 729 CTACTATGTTGCCAATATTTCTCTGCTGTAATATATGATGAAGAATATACCCGTA 788
Oy 198 rGluGlnGlyAlaProCysAlaSerCysProAspAsnGlyLeuCysThrAs 218
Db 789 CCACAAAGAACACCTTGTGCGGTTGCCGTGATGACTGTACAAAGACATATGACACCA 848

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XX 16-SEP-2002 (first entry)
DT
XX Human prostate expression marker CDNA 43205.
DE
XX Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KM pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
PN
XX WO200160860-A2.
XX
XX 23-AUG-2001.
PD
XX
XX 20-FEB-2001; 2001WO-US05171.
PF
XX 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
XX Schlegel R, Endege WO, Monahan JE;
PI
XX WPI; 2001-662795/76.
DR
XX
XX Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX
XX
XX Claim 1; Page 8623; 11750pp; English.

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

Sequence 534 BP; 120 A; 127 C; 133 G; 153 T; 1 other:
XX
XX

Alignment Scores:

Pred. No.:	1.87e-60	Length:	534
Score:	683.00 <td>Matches:</td> <td>132</td>	Matches:	132
Percent Similarity:	98.51%	Conservative:	0
Best Local Similarity:	98.51%	Mismatches:	1
Query Match:	47.56%	Indels:	1
DB:	23	Gaps:	0

US-09-698-761-3 (1-258) x ABV43214 (1-534)

1 MetLysGlnIleLeuHisProAlaLeuGluThrThrAlaMetThrLeuPheProValLeu 20
ATGAAACCAATATCTTCACTCTGCTGGAAACCACTGCATGACATTATTCGCCAGTGTG 375
434

21 LeuPheValAlaGlyLeuLeuProSerPheProAlaAsnGluAspLysAspProAla 40
TTGTTCTGCTGCTGGGCGCTTCATCTTTCCACCAATGAGATAGGATCCCGCT 315
374

41 PheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLysHisAsn 60
TTTCTTCTGCTGCTGGGCGCTTCATCTTTCCACCAATGAGATAGGATCCCGCT 315

Db	314	TTTACTGTTTGTAAACCAACCAACACAGTGCAGAAAGGAGATTTGTAATAAGCAAT	255
QY	61	GLULeuArgrAlaValSerProFroAlaArGaSnMetLeuLysMetLutrrpAsnLys	80
Db	254	GAACGTGAGAGAGACAGTATCTCCCTCCGACAAACATGCTTAAGTGGAAATGGAACAA	195
QY	81	GLUAlaAlaAlaAsnAlaGlnLysTrpAlaAsn-GlnCysAsnTYrArGHisSerAsnPr	100
Db	194	GAGCGTCAGCAAAATGCCCAAAAGTGGGCAAAACNCRAGTGCATTTACAGACACAGTAACCC	135
QY	100	OLysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTYrMetSerSerAlaProSe	120
Db	134	AAAGATGTCGATGACACAGTCTTAATGTGTGATGAGATCTCTACATGTCAAGTGCCCTCAG	75
QY	120	rSerTrpSerGlnAlaAlaIleGlnSerTrpPheAspGluTYr	133
Db	74	CTCATGTCACACAGCAATCCAAACCTGGTTGTATGAGTAC	35
RESULT 15			
AAST0842			
Db	AAST0842	standard; cDNA; 663 BP.	
AC	AAST0842;		
XX	13-FEB-2002	(first entry)	
XX			
DE		DNA encoding novel human diagnostic protein #6646.	
XX			
KW		Human: chromosome mapping; gene mapping; gene therapy; forensic;	
KM		food supplement; medical imaging; diagnostic; genetic disorder; ss.	
XX			
OS		Homo sapiens.	
XX			
PN	WO200175067-A2.		
PD	11-OCT-2001.		
XX			
PF	30-MAR-2001; 2001WO-US08631.		
XX			
PR	31-MAR-2000; 2000US-0540217.		
XX			
PR	23-AUG-2000; 2000US-0649167.		
XX			
PA	(HXSE-) HXSEQ INC.		
XX			
PI	Dmanac RT, Liu C, Tang YT;		
XX			
DR	WPI: 2001-639362/73.		
XX			
DR	P-PSDB; ABG06655.		
XX			
PT		New isolated polynucleotide and encoded polypeptides, useful in	
XX		diagnostics, forensics, gene mapping, identification of mutations	
PT		responsible for genetic disorders or other traits and to assess	
XX		biodiversity	
XX			
PS	Claim 1; SEQ ID No 6646; 103bp; English.		
XX			
CC		The invention relates to isolated polynucleotide (I) and	
CC		polypeptide (II) sequences. (I) is useful as hybridization probes,	
CC		polymerase chain reaction (PCR) primers, oligomers, and for chromosome	
CC		and gene mapping, and in recombinant production of (II). The	
CC		polynucleotides are also used in diagnostics as expressed sequence tags	
CC		for identifying expressed genes. (I) is useful in gene therapy techniques	
CC		to restore normal activity of (II) or to treat disease states involving	
CC		(II). (II) is useful for generating antibodies against it, detecting or	
CC		quantitating a polypeptide in tissue, as molecular weight markers and as	
CC		a food supplement. (II) and its binding partners are useful in medical	
CC		imaging of sites expressing (II). (I) and (II) are useful for treating	
CC		disorders involving aberrant protein expression or biological activity.	
CC		The polypeptide and polynucleotide sequences have applications in	
CC		diagnostics, forensics, gene mapping, identification of mutations	
CC		responsible for genetic disorders or other traits to assess biodiversity	
CC		and to produce other types of data and products dependent on DNA and	
CC		amino acid sequences. AAS64197-AAS94364 represent novel human	

CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX

SQ Sequence 683 BP; 215 A; 165 C; 141 G; 162 T; 0 other;

Alignment Scores:

Prod. No.:	2.98e-45	Length:	683
Score:	535.50	Matches:	119
Percent Similarity:	64.73%	Conservative:	15
Best Local Similarity:	57.49%	Mismatches:	31
Query Match:	37.29%	Indels:	44
DB:	23	Gaps:	4

US-09-698-781-3 (1-258) x AAST0842 (1-683)

```
OY 1 MetLysGlnIleLeuHisProAlaLeuGluThr-TThr-----AlaMetThrLeuPhePr 18
   ::::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 ATAAAGTAGATATTTCATCTCTGCTCAGAAACACACATTTCAGACATGGCTTTACTACC 236
OY 18 oValLeuLeuPheLeuValAlaIleLeuLeuProSerPheProAlaAsnGlnAspLysAs 38
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 237 GGTG---TTGTTCTGTGTTACTGCTGCTGCTGCTTCATCTTACTGCA---GAAGGAAAGCA 290
OY 38 ProAlaPheThrAlaLeuLeuThrThrGlnThrGlnValGlnArgGluIleValAsnLys 58
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 291 TCCCGCTTTACTGCTTTGTTTACCCACCCAGTTGCACAAAGGAGATGTAATAA 350
OY 58 sHisAsnGluLeuArgArgAlaValAlaSerProAlaArgAsnMetLeuLysMetGluTr 78
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 351 ACACAAATGAACTAGAGAAAGCACTCTCCACTGCCAGTACATGCTAAAGATGGAATG 410
OY 78 pAsnLysGlnAlaAlaAlaAsnAlaGlnLysTrpAlaAsnGlnCysAsnTrpArgHisSe 98
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 411 GAGCAGAGAGGTAAACAGCAATGCCCAAGGTGGCAACAACTCACTTACAA-CATAG 469
OY 98 rAsnProLysAspArgMetThrSerLeuLysCysGlyGluAsnLeuTrpMetSerAl 118
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 470 TGATCCAGAGGAGCCGAAACAGTACAAAGATGTTGAGAAATCTATATGTCAAGTGA 529
OY 118 aProSerSerTrpSerGlnAlaAlaIleGlnInsertPrpPheAspGluTrpAsnAspPheAsp 138
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 530 CCTTACTCTCTGCTCTTCTGCAATCCAAAGCTGGTATGACGAGATCCTAGATTGTGCTA 589
OY 138 eGlyValGlyProLysThrProAsnAlaValAlaGlyHisIleIleValAlaValTrypt 158
   ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 590 TGCTGTAGAGACCAAGAGTCCCA----- 613
OY 158 rSerSerTrpLeuValGlyCysGlyAsnAlaTrpCysProAsnGlnLysValLeuLysTrp 178
   ::| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 613 ----- 613
OY 178 rTyrTrpValCysGlnTrpCysProAlaGlnAsnTrpAlaAsnArgLeuTrpValProTy 198
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 614 -----TATGTCTCTGCTGTAATATATGAAATAGAAAGATATACCCCGTA 657
OY 198 rGlnGlnGlyAlaProCys 204
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 658 CCACAGAGGAGACACCTGT 676
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Search completed: March 14, 2003, 03:17:52
Job time : 393.449 secs